

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

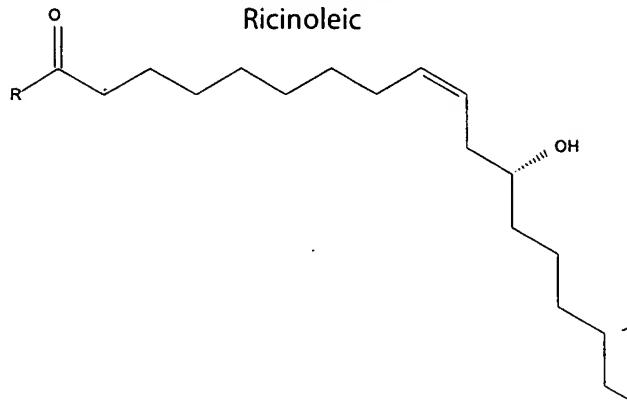
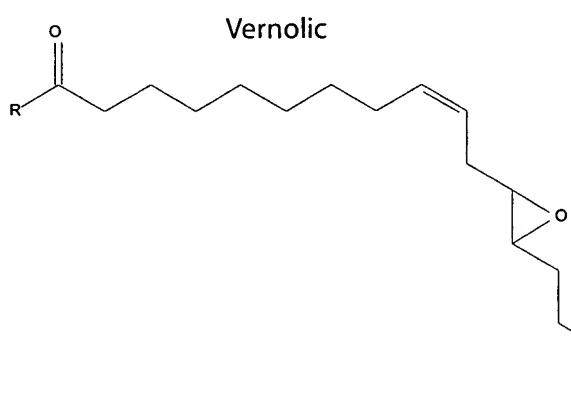
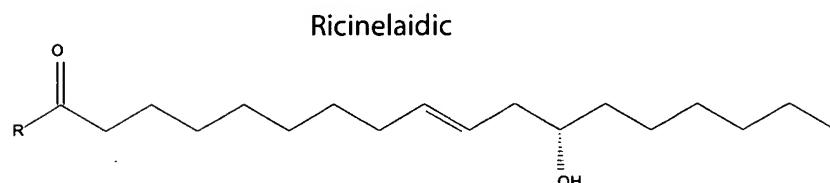
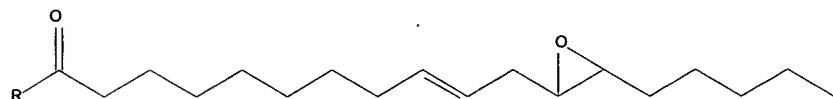


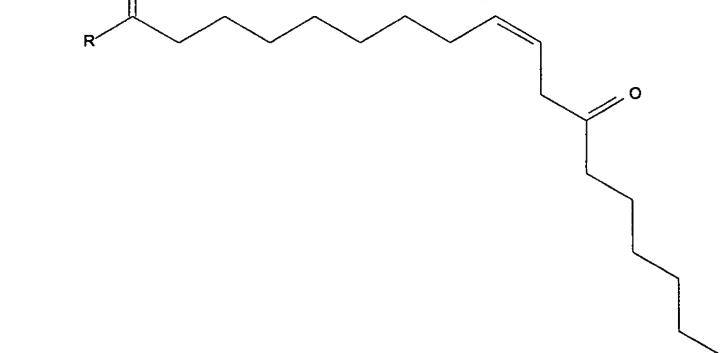
FIG. 1



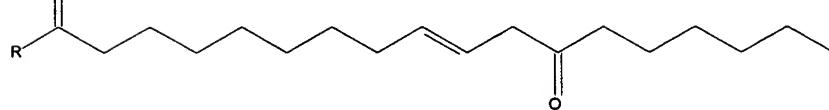
12,13-epoxy-trans-9-octadecenoic



12-oxo-cis-9-octadecenoic



12-oxo-trans-9-octadecenoic



## NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND PLANTS MADE THEREFROM

Michelle L. Verbsky et al.

12557-016001

SEQ_ID	NO	37	MASSGRMSTVITSNNSEKKGG-SSHLKRAPHTKPPFTGLDLKRAIIPHCPERSFVRSPFSVYAVDVCLSLFLFYSIATNFPYISSLPS-XVANLVWYLF	96
SEQ_ID	NO	39	MASSGRMSTVITSNNSEKKGG-SSHLKRAPHTKPPFTGLDLKRAIIPHCPERSFVRSPFSVYAVDVCLSLFLFYSIATNFPYISSLPS-XVANLVWYLF	96
SEQ_ID	NO	13	MGGGGRMSTVITSNNSEKKGG-SSHLKRAPHTKPPFTGLDLKRAIIPHCPERSFVRSPFSVYAVDVCLSLFLFYSIATNFPYISSLPS-XVANLVWYLF	96
SEQ_ID	NO	34	MGGGGRMSTVITSNNSE--SSHLKRAPHTKPPFTGLDLKRAIIPHCPERSFVRSPFSVYAVDVCLSLFLFYSIATNFPYISSLPS-XVANLVWYLF	92
SEQ_ID	NO	19	MAGAGRMPVTSSSKS--TDTTKRCPCEKKPFVSPGSVLDLKKAIIPHCPERSFVRSPFSVYAVDVCLSLFLFYSIATNFPYISSLPS-XVANLVWYLF	92
SEQ_ID	NO	127	MAGAGRRTDWPVPAKNSK--VDPLKRVPFEKFOPLSQSLQSKKAIIPHCPERSFVRSPFSVYAVDVCLSLFLFYSIATNFPYISSLPS-XVANLVWYLF	92
SEQ_ID	NO	128	MAGAGRMSDPTTNDKEQR--KNPQLRQPVYAKRPPFTGLDIKKAIIPHCPERSFVRSPFSVYAVDVCLSLFLFYSIATNFPYISSLPS-YLAWPLYWAV	92
SEQ_ID	NO	17	MAGAGRIMVTPSKSKS--TEALKRGCPCEKKPFVTPDKLKKAIIPQHCPQRSPRSFSYLLTDITLVSCFVYVATNYSFLSLPQPLSTLYAWPLYWVC	93
SEQ_ID	NO	35	MAGAGRIMVTPSKSKS--TEALKRGCPCEKKPFVTPDKLKKAIIPQHCPQRSPRSFSYLLTDITLVSCFVYVATNYSFLSLPQPLSTLYAWPLYWVC	92
SEQ_ID	NO	40	MASSGRMVTSSSKS--TEALKRGCPCEKKPFVTPDKLKKAIIPQHCPQRSPRSFSYLLTDITLVSCFVYVATNYSFLSLPQPLSTLYAWPLYWVC	93
SEQ_ID	NO	14	MAGAGRIMVTSSSKS--TEALKRGCPCEKKPFVTPDKLKKAIIPQHCPQRSPRSFSYLLTDITLVSCFVYVATNYSFLSLPQPLSTLYAWPLYWVC	93
SEQ_ID	NO	20	MAGAGRMPVTSSSKS--TDTTKRCPCEKKPFVSPGSVLDLKKAIIPQHCPQRSPRSFSYLLTDITLVSCFVYVATNYSFLSLPQPLSTLYAWPLYWVC	93
SEQ_ID	NO	23	MAGAGRMPVTSSSKS--TDTTKRCPCEKKPFVSPGSVLDLKKAIIPQHCPQRSPRSFSYLLTDITLVSCFVYVATNYSFLSLPQPLSTLYAWPLYWVC	93
SEQ_ID	NO	15	MAGAGRIMVTSSSKS--PEALRRGPGEKKPFVQDRLKAIIPRHCPEKRSIPRSFSYLLTDIILASCFYVYVATNYSFLSLPQPLSTYFWAPLYWVC	93
SEQ_ID	NO	21	MAGAGRMPVTSSSKS--TDTTKRCPCEKKPFVSPGSVLDLKKAIIPRHCPEKRSIPRSFSYLLTDIILASCFYVYVATNYSFLSLPQPLSTYFWAPLYWVC	93
SEQ_ID	NO	16	MAGAGRIMVTSSSKS--PQALRRGPCEKKPFVTPDKLKKAIIPQHCPQRSPRSFSYLLTDITLVSCFVYVATNYSFLSLPQPVSNLYAWPLYWIC	93
SEQ_ID	NO	22	MAGAGRMPVTSSSKS--TDTTKRCPCEKKPFVSPGSVLDLKKAIIPHCPEKRSIPRSFSYLLTDITLVSCFVYVATNYSFLSLPQPVSNLYAWPLYWIC	93
SEQ_ID	NO	125	MAGAGRMPVTSSSKS--TDTTKRCPCEKKPFVSPGSVLDLKKAIIPHCPEKRSIPRSFSYLLTDIILASCFYVYVATNYSFLSLPQPLS-YLAWPLYWAC	92
SEQ_ID	NO	126	MAGAGRMRQMVSPPSKS--TDTTKRCPCECTPPTVGBLKKAIIPHCPEKRSIPRSFSYLLTDIILASCFYVYVATNYSFLSLPQPLS-YLAWPLYWAC	92
SEQ_ID	NO	18	MGAHG---HGRTSK--KSVMERVSVDVPVFSLSLDLKKAIIPHCPERSFVRSSYYVHDLLIAYIFYLADKYIIP1LPAPLA-YLAWPLYWFC	86
SEQ_ID	NO	41	MASSG---HSRTSK--KSVMERVSVDVPVFSLSLDLKKAIIPHCPERSFVRSSYYVHDLLIAYIFYLADKYIIP1LPAPLA-YLAWPLYWFC	86
SEQ_ID	NO	24	MAGAGRMPVTSSSKS--TDTTKRCPCEKKPFVSPGSVLDLKKAIIPHCPERSFVRSSYYVHDLLIAYIFYLADKYIIP1LPAPLA-YLAWPLYWFC	92
SEQ_ID	NO	38	MASSGR---MSDLSDG--KNLLKRVVPDP--PFTLSDIKKAIIPHCPEKRSVRSPFSVYVFFPLATTYITVLPAPLA-YIAPWVVFYWC	87
SEQ_ID	NO	42	MASSGR---MSDLSDG--KNLLKRVVPDP--PFTLSDIKKAIIPHCPEKRSVRSPFSVYVFFPLATTYITVLPAPLA-YIAPWVVFYWC	87
SEQ_ID	NO	36	MAGAGR---MSDLSDG--KNLLKRVVPDP--PFTLSDIKKAIIPHCPEKRSVRSPFSVYVFFPLATTYITVLPAPLA-YIAPVYWF	87

SEQ_ID	NO_37	PLYLA FNV SGRPYD R-FAC HYDPYGP I-FIS ERLQIY IA DLGI PAT TFLV YQAT MAK GLA WV M R I Y G V P L I V N C P L V M I T Y L Q H T H P A I P R Y G S S E W	291
SEQ_ID	NO_39	PLYLA FNV SGRPYD R-FAC HYDPYGP I-FIS ERLQIY IA DLGI PAT TFLV YQAT MAK GLA WV M R I Y G V P L I V N C P L V M I T Y L Q H T H P A I P R Y G S S E W	291
SEQ_ID	NO_13	PLYLA FNV SGRPYD R-FAC HYDPYGP I-FIS ERLQIY IA DLGI PAT TFLV YQAT MAK GLA WV M R I Y G V P L I V N C P L V M I T Y L Q H T H P A I P R Y G S S E W	291
SEQ_ID	NO_34	PLYLA FNV SGRPYD R-FAC HYDPYGP I-FIS ERLQIY IA DLGI PAT TFLV YQAT MAK GLA WV M R I Y G V P L I V N C P L V M I T Y L Q H T H P A I P R Y G S S E W	287
SEQ_ID	NO_19	PLYLA FNV SGRPYD R-FAC HYDPYGP I-FIS ERLQIY IA DLGI PAT TFLV YQAT MAK GLA WV M R I Y G V P L I V N C P L V M I T Y L Q H T H P A I P R Y G S S E W	287
SEQ_ID	NO_127	PLYLA FNV SGRPYD R-FAC HYDPYGP I-FIS ERLQIY IA DLGI PAT TFLV YQAT MAK GLA WV M R I Y G V P L I V N C P L V M I T Y L Q H T H P A I P R Y G S S E W	287
SEQ_ID	NO_128	PLYLF N SGRPYD R-FAC HD FPYGP IYND FIS ERLQI DAG I IA AV CV Y R V A L G W L C V Y G P L I V N G F L P L H T P S L P H Y D S S E W	287
SEQ_ID	NO_17	PLYLA FNV SGRPYD G-FAS HFFPH AP IFKD ERLQIY ISD AG I IA AV CV Y R V A L G W L C V Y G P L I V N F L V F L Q H T H P S L P H Y D S T E W	288
SEQ_ID	NO_35	PLYLA FNV SGRPYD G-FAS HFFPH AP IFKD ERLQIY ISD AG I IA AV CV Y R V A L G W L C V Y G P L I V N F L V F L Q H T H P S L P H Y D S T E W	288
SEQ_ID	NO_40	PLYLA FNV SGRPYD G-FAS HFFPH AP IFKD ERLQIY ISD AG I IA AV CV Y R V A L G W L C V Y G P L I V N F L V F L Q H T H P S L P H Y D S T E W	288
SEQ_ID	NO_14	PLYLP FNV SGRPYD G-FAS HFFPH AP IFKD ERLQIY ISD AG I IA AV CV Y R V A L G W L C V Y G P L I V N F L V F L Q H T H P S L P H Y D S T E W	288
SEQ_ID	NO_20	PLYLP FNV SGRPYD G-FAS HFFPH AP IFKD ERLQIY ISD AG I IA AV CV Y R V A L G W L C V Y G P L I V N F L V F L Q H T H P S L P H Y D S T E W	288
SEQ_ID	NO_23	PLYLA FNV SGRPYD G-FAS HFFPH AP IFKD ERLQIY ISD AG I IA AV CV Y R V A L G W L C V Y G P L I V N F L V F L Q H T H P S L P H Y D S T E W	288
SEQ_ID	NO_15	PLYLA FNV SGRSYD G-FAS HFFPH AP IFKD ERLQIY H I Y T D A G I A V C Y G P L I V N F L V F L Q H T H P S L P H Y D S T E W	288
SEQ_ID	NO_21	PLYLA FNV SGRSYD G-FAS HFFPH AP IFKD ERLQIY H I Y T D A G I A V C Y G P L I V N F L V F L Q H T H P S L P H Y D S T E W	288
SEQ_ID	NO_16	PLYLA FNV SGRSYD G-FAS HFFPH AP IFKD ERLQIY H I Y T D A G I A V C Y G P L I V N F L V F L Q H T H P S L P H Y D S T E W	288
SEQ_ID	NO_22	PLYLA FNV SGRPYD G-FAS HFFPH AP IFKD ERLQIY H I Y T D A G I A V C Y G P L I V N F L V F L Q H T H P S L P H Y D S T E W	288
SEQ_ID	NO_125	PLYLA FNV SGRPYD G-FAS HFFPH AP IFKD ERLQIY H I Y T D A G I A V C Y G P L I V N F L V F L Q H T H P S L P H Y D S S E W	288
SEQ_ID	NO_126	PLYLA FNV SGRPYD G-FAS HFFPH AP IFKD ERLQIY H I Y T D A G I A V C Y G P L I V N F L V F L Q H T H P S L P H Y D S S E W	288
SEQ_ID	NO_18	PLYLL TN ISGKKYD R-FAN HFDP MSPI F K R E R F Q V L S D L G L L A V F Y G I K V A A V G A A V C M Y G P M L G V F T L F D I I T L H H T Q S S P H Y D S T E W	281
SEQ_ID	NO_41	PLYLL TN ISGKKYD R-FAN HFDP MSPI F K R E R F Q V L S D L G L L A V F Y G I K V A A V G A A V C M Y G P M L G V F T L F D I I T L H H T Q S S P H Y D S T E W	287
SEQ_ID	NO_24	PLYLL TN ISGKKYD R-FAN HFDP MSPI F K R E R F Q V L S D L G L L A V F Y G I K V A A V G A A V C M Y G P M L G V F T L F D I I T L H H T Q S S P H Y D S T E W	287
SEQ_ID	NO_38	PLYLL TN ISGKKYD R-FAN HFDP MSPI F K R E R F Q V L S D L G L L A V F Y G I K V A A V G A A V C M Y G P M L G V F T L F D I I T L H H T Q S S P H Y D S T E W	282
SEQ_ID	NO_42	PLYLL TN ISGKKYD R-FAN HFDP MSPI F K R E R F Q V L S D L G L L A V F Y G I K V A A V G A A V C M Y G P M L G V F T L F D I I T L H H T Q S S P H Y D S T E W	282
SEQ_ID	NO_36	PLYLL TN ISGKKYD R-FAN HFDP MSPI F K R E R F Q V L S D L G L L A V F Y G I K V A A V G A A V C M Y G P M L G V F T L F D I I T L H H T Q S S P H Y D S T E W	282

FIG. 2-1

SEQ_ID_NO	rule	37	DWLRGAMTVDRDYGLNLKVPHNIAIDTVAHHLFATVPHYNAMEATAIKPIMGFYRYDGTPFYKALWREAKECLFVFPDEGAFTQGVFWYRNKY	387
SEQ_ID_NO	39	DWLRGAMTVDRDYGLNLKVPHNIAIDTVAHHLFATVPHYNAMEATAIKPIMGFYRYDGTPFYKALWREAKECLFVFPDEGAFTQGVFWYRNKY	387	
SEQ_ID_NO	13	DWLRGAMTVDRDYGLNLKVPHNIAIDTVAHHLFATVPHYNAMEATAIKPIMGFYRYDGTPFYKALWREAKECLFVFPDEGAFTQGVFWYRNKY	387	
SEQ_ID_NO	34	DWLRGAMTVDRDYGLNLKVPHNIAIDTVAHHLFATVPHYNAMEATAIKPIMGFYRYDGTPFYKALWREAKECLFVFPDEGAFTQGVFWYRNKY	383	
SEQ_ID_NO	19	DWLRGAMTVDRDYGLNLKVPHNIAIDTVAHHLFATVPHYNAMEATAIKPIMGFYRYDGTPFYKALWREAKECLFVFPDEGAFTQGVFWYRNKY	383	
SEQ_ID_NO	127	DWLRGALATVDRDYGLNLKVPHNITDTVAHHLFATVPHYNAMEATAIKPILGEGYYRFDGTTPFKALWREAKECLFVFPDEGAFTQGVFWYRNKY	383	
SEQ_ID_NO	128	DWLRGALATVDRDYGLNLKVPHNITDTVAHHLFATVPHYNAMEATAIKPILGEGYYRFDGTTPFKAMWREAKECLFVFPDEGAFTQGVFWYNNKL	383	
SEQ_ID_NO	17	EWIRGALVTVDRDYGLNLKVPHNITDTVAHHLFATIIPHNAMEATEAIKPILGDYYHFDGTPWVYAMYREAKECLFVFPDETERGKKGVYYYYNNKL	384	
SEQ_ID_NO	35	EWIRGALVTVDRDYGLNLKVPHNITDTVAHHLFATIIPHNAMEATEAIKPILGDYYHFDGTPWVYAMYREAKECLFVFPDETERGKKGVYYYYNNKL	383	
SEQ_ID_NO	40	EWIRGALVTVDRDYGLNLKVPHNITDTVAHHLFATIIPHNAMEATEAIKPILGDYYHFDGTPWVYAMYREAKECLFVFPDETERGKKGVYYYYNNKL	384	
SEQ_ID_NO	14	EWIRGALVTVDRDYGLNLKVPHNITDTVAHHLFATIIPHNAMEATEAIKPILGDYYHFDGTPWVYAMYREAKECLFVFPDETERGKKGVYYYYNNKL	384	
SEQ_ID_NO	20	EWIRGALVTVDRDYGLNLKVPHNITDTVAHHLFATIIPHNAMEATEAIKPILGDYYHFDGTPWVYAMYREAKECLFVFPDETERGKKGVYYYYNNKL	384	
SEQ_ID_NO	23	EWIRGALVTVDRDYGLNLKVPHNITDTVAHHLFATIIPHNAMEATEAIKPILGDYYHFDGTPWVYAMYREAKECLFVFPDETERGKKGVYYYYNNKL	384	
SEQ_ID_NO	15	DWIRGAMTVDRDYGLNLKVPHNITDTVAHHLFATIIPHNAMEATEAIKPILGDYYHFDGTPWVYAMYREAKECQLVYEQDTEK-KGGGVYYYYNNKL	383	
SEQ_ID_NO	21	DWIRGAMTVDRDYGLNLKVPHNITDTVAHHLFATIIPHNAMEATEAIKPILGDYYHFDGTPWVYAMYREAKECQLVYEQDTEK-KGGGVYYYYNNKL	384	
SEQ_ID_NO	16	EWIRGALVTVDRDYGLNLKVPHNITDTVAHHLFATIIPHNAMEATEAIKPILGDYYHFDGTPWVYAMYREAKECLFVFPDETERGKKGVYYYYNNKL	384	
SEQ_ID_NO	22	EWIRGALVTVDRDYGLNLKVPHNITDTVAHHLFATIIPHNAMEATEAIKPILGDYYHFDGTPWVYAMYREAKECLFVFPDETERGKKGVYYYYNNKL	384	
SEQ_ID_NO	125	DWLRGALATVDRDYGLNLKVPHNITDTVAHHLFSTMPHYNAMEATAIKPILGDYYHFDGTPWVYAMYREAKECLFVFPDEGAFTQGVFWYNNKL	383	
SEQ_ID_NO	126	DWLRGALATVDRDYGLNLKVPHNITDTVAHHLFSTMPHYNAMEATAIKPILGDYYHFDGTPWVYAMYREAKECLFVFPDEGAFTQGVFWYNNKL	384	
SEQ_ID_NO	18	NWIRGALSAIDRDFGFMNSVPEDVTHTHVMMHMPSYIPHAKEARDAINTIIGDYMIDRTPILKALWREAKECMYP1EPD--SKRGKGVWYHKL-	374	
SEQ_ID_NO	41	NWIRGALSAIDRDFGFMNSVPEDVTHTHVMMHMPSYIPHAKEARDAINTIIGDYMIDRTPILKALWREAKECMYP1EPD--SKRGKGVWYHKL-	374	
SEQ_ID_NO	24	NWIRGALSAIDRDFGFMNSVPEDVTHTHVMMHMPSYIPHAKEARDAINTIIGDYMIDRTPILKALWREAKECMYP1EPD--SKRGKGVWYHKL-	380	
SEQ_ID_NO	38	NWIRGALSTIDRDFGFLNRLRVFHVDVTHTVLHLISYIPHAKEARDAIKPVLGDYYKIDRTPIFKAMWREAKECIYIIPDDETEHKGVWYHKM-	377	
SEQ_ID_NO	42	NWIRGALSTIDRDFGFLNRLRVFHVDVTHTVLHLISYIPHAKEARDAIKPVLGDYYKIDRTPIFKAMWREAKECIYIIPDDETEHKGVWYHKM-	377	
SEQ_ID_NO	36	NWIRGALSTIDRDFGFLNRLRVFHVDVTHTVLHLISYIPHAKEARDAIKPVLGDYYKIDRTPIFKAMWREAKECIYIIPDDETEHKGVWYHKM-	377	

**FIG. 2-2**

# Expression Constructs

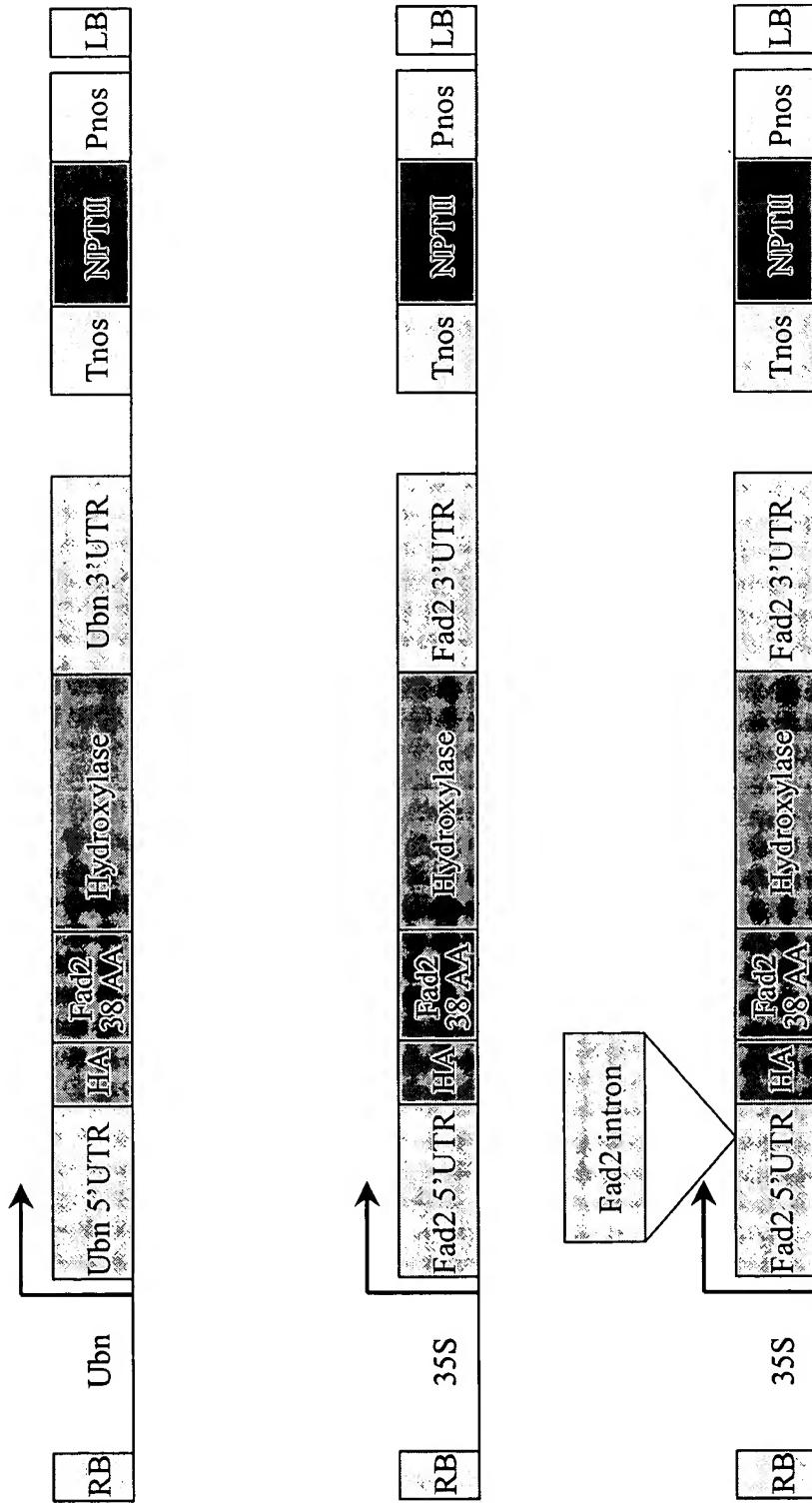


FIG. 3

FIG. 4

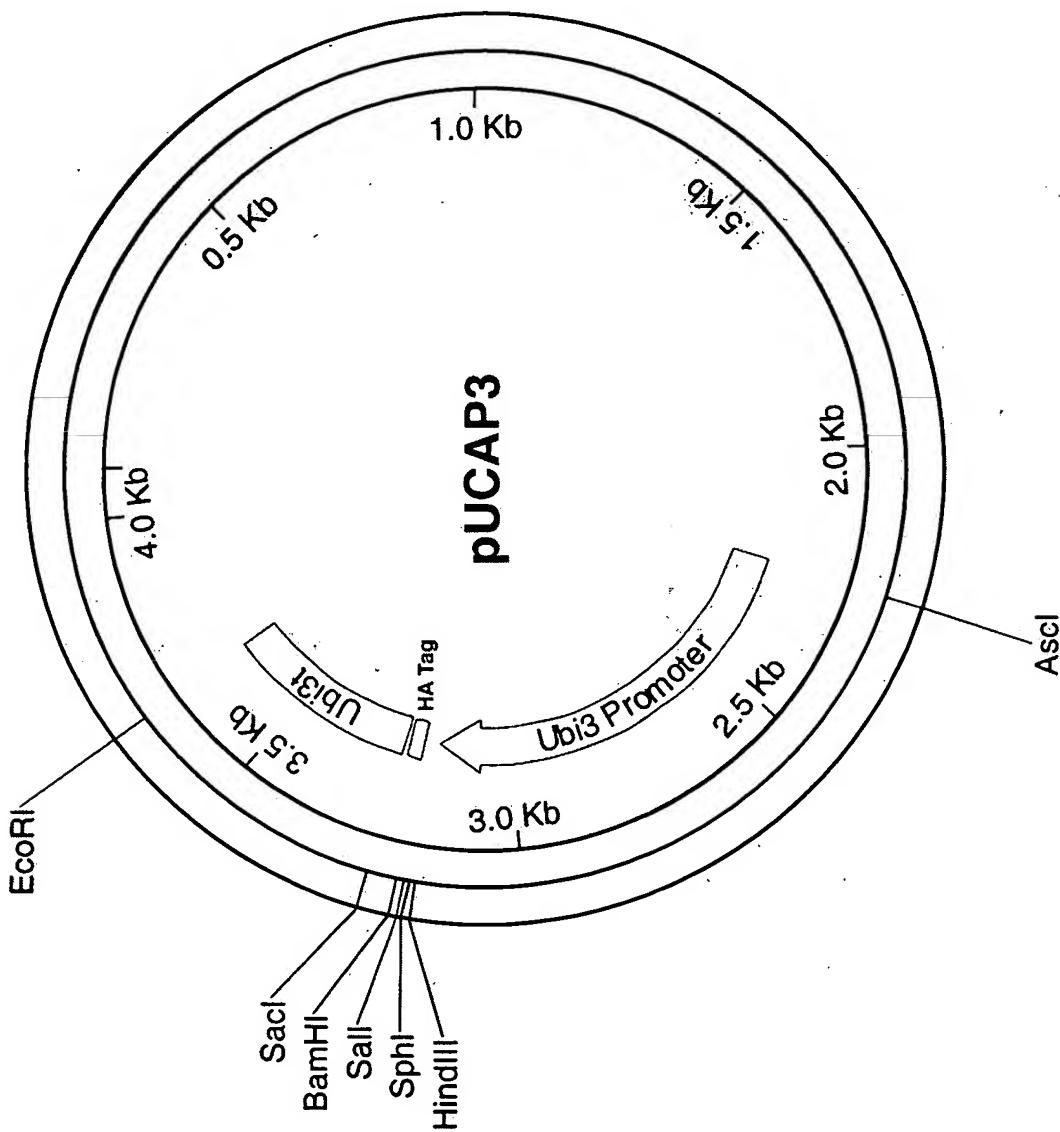


FIG. 5

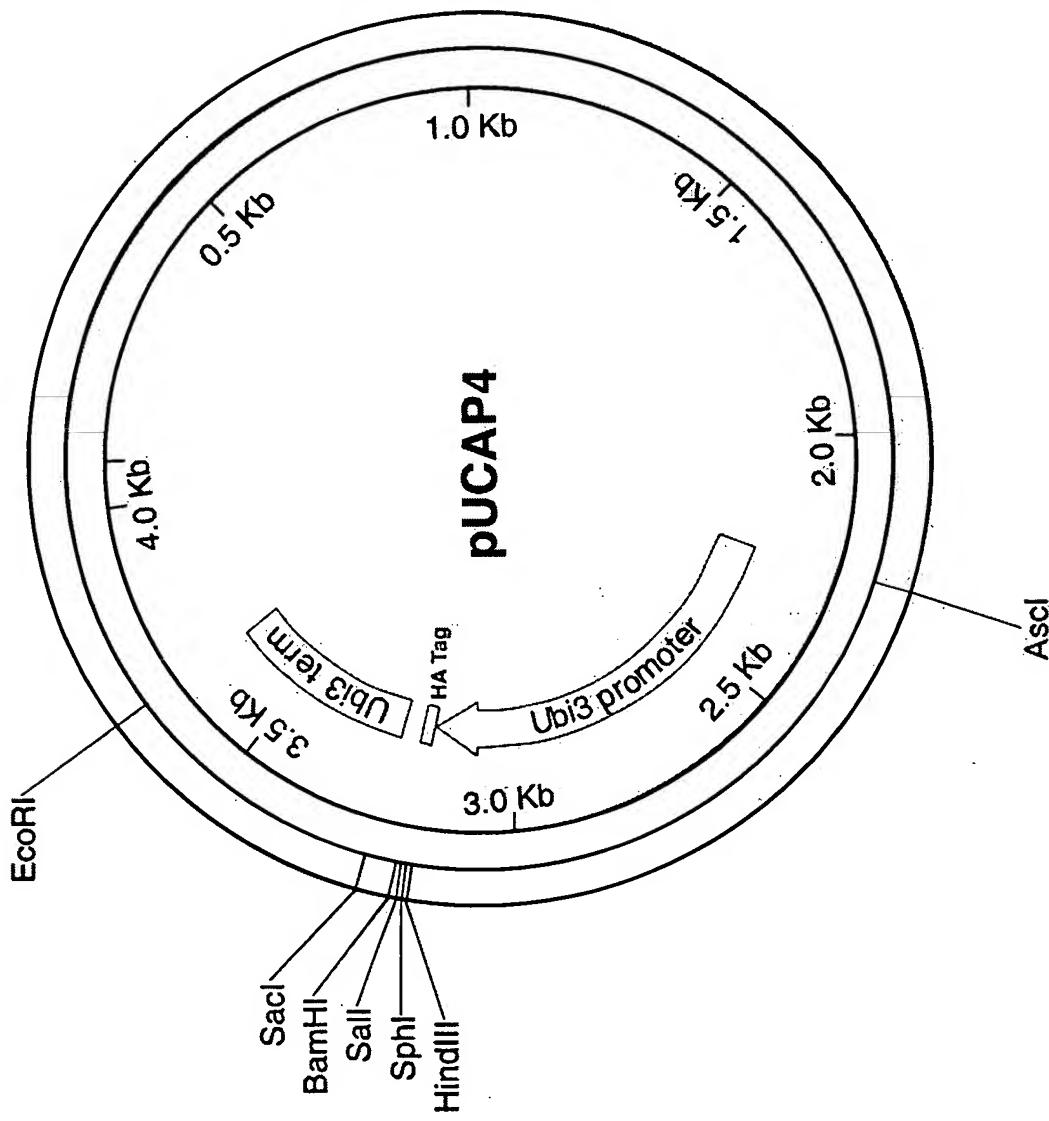


FIG. 6

